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=> 11 and (array or microarray) L2 2967 L1 AND (ARRAY OR MICROARRAY)

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=> 13 and muscle

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L6 ANSWER 1 OF 24 MEDLINE on STN

TI Cross-species hybridisation of **pig** RNA to human nylon microarrays.

L6 ANSWER 2 OF 24 MEDLINE on STN

- TI Ascaris suum: cDNA microarray analysis of 4th stage larvae (L4) during self-cure from the intestine.
- L6 ANSWER 3 OF 24 MEDLINE on STN

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- TI Leptin receptor-deficient Zucker (fa/fa) rat retards the development of pig serum-induced liver fibrosis with Kupffer cell dysfunction.
- L6 ANSWER 4 OF 24 MEDLINE on STN
- TI Complementary DNA macroarray analyses of differential gene expression in **porcine** fetal and postnatal **muscle**.
- L6 ANSWER 5 OF 24 MEDLINE on STN
- TI Development of a **porcine** skeletal **muscle cDNA microarray**: analysis of differential transcript expression in phenotypically distinct **muscles**.
- L6 ANSWER 6 OF 24 MEDLINE on STN
- TI Generation of expressed sequence tags from a normalized porcine skeletal muscle cDNA library.
- L6 ANSWER 7 OF 24 MEDLINE on STN
- TI The biology of somatotropin in adipose tissue growth and nutrient partitioning.
- L6 ANSWER 8 OF 24 MEDLINE on STN
- TI The GalR2 galanin receptor mediates galanin-induced jejunal contraction, but not feeding behavior, in the rat: differentiation of central and peripheral effects of receptor subtype activation.
- L6 ANSWER 9 OF 24 MEDLINE on STN
- TI Structure of tropomyosin at 9 angstroms resolution.
- L6 ANSWER 10 OF 24 CABA COPYRIGHT 2006 CABI on STN
- TI Cross-species hybridisation of **pig** RNA to human nylon microarrays.
- L6 ANSWER 11 OF 24 CABA COPYRIGHT 2006 CABI on STN
- TI The biology of somatotropin in adipose tissue growth and nutrient partitioning.
- L6 ANSWER 12 OF 24 CAPLUS COPYRIGHT 2006 ACS on STN
- TI Genes expressed in atherosclerotic tissue and their use in diagnosis and pharmacogenetics
- L6 ANSWER 13 OF 24 CAPLUS COPYRIGHT 2006 ACS on STN
- TI Identification of candidate genes and proteins related to human atherosclerosis susceptibility locus (ATHS) and genetic markers for atherosclerosis prediction
- L6 ANSWER 14 OF 24 CAPLUS COPYRIGHT 2006 ACS on STN
- TI Genes showing altered patterns of expression in multiple sclerosis and their diagnostic and therapeutic uses
- L6 ANSWER 15 OF 24 CAPLUS COPYRIGHT 2006 ACS on STN
- TI Novel pharmaceutical composition of interferon gamma or pirfenidone combined with molecular diagnostics for the improved treatment of interstitial lung diseases
- L6 ANSWER 16 OF 24 CAPLUS COPYRIGHT 2006 ACS on STN
- TI Muscle-specific F-box protein, atrogin-1, highly expressed during muscle atrophy, and compositions and methods for diagnosis and treatment of muscle wasting
- L6 ANSWER 17 OF 24 CAPLUS COPYRIGHT 2006 ACS on STN

- TI Development of a porcine skeletal muscle cDNA microarray: analysis of differential transcript expression in phenotypically distinct muscles
- L6 ANSWER 18 OF 24 CAPLUS COPYRIGHT 2006 ACS on STN
- TI Cell-specific gene expression profiles and algorithms for their construction and their uses for determining the phenotype of cells and distinguishing cell lines
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- Identification of proacrosin binding protein sp32 precursor as a human TI cancer/testis antigen
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- Leptin receptor-deficient Zucker (fa/fa) rat retards the development of ΤI pig serum-induced liver fibosis with Kupffer cell dysfunction.
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- TI A Comparison of Porcine Ocular Tissue Gene Expression by Microarray Analysis.
- ANSWER 22 OF 24 DISSABS COPYRIGHT (C) 2006 ProQuest Information and 1.6 Learning Company; All Rights Reserved on STN
- TI Molecular, genetic and physical mapping of the porcine genome
- ANSWER 23 OF 24 EMBASE COPYRIGHT (c) 2006 Elsevier B.V. All rights L6 reserved on STN
- TI Cross-species hybridisation of pig RNA to human nylon microarrays.
- ANSWER 24 OF 24 EMBASE COPYRIGHT (c) 2006 Elsevier B.V. All rights L6 reserved on STN
- ΤI Development of a porcine skeletal muscle cDNA microarray: Analysis of differential transcript expression in phenotypically distinct muscles.

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L7 24 DUP REM L6 (0 DUPLICATES REMOVED)

=> d 16 10, 1, 6, 21 ibib abs

ANSWER 10 OF 24 CABA COPYRIGHT 2006 CABI on STN

ACCESSION NUMBER:

2004:172135 CABA

DOCUMENT NUMBER:

20043153082

TITLE:

Cross-species hybridisation of pig RNA to

human nylon microarrays

AUTHOR:

Moody, D. E.; Zou, Z.; McIntyre, L.

CORPORATE SOURCE:

Department of Animal Science, 1151 Lilly Hall, Purdue University, West Lafayette, IN 47907, USA. moodyd@purdue.edu; chenwei.tseng@mesanetworks.net;

lmcintyre@purdue.edu

SOURCE:

BMC Genomics, (2002) Vol. 3, No. 27, pp. (27 September 2002). 15 ref.

Publisher: BioMed Central Ltd. London

ISSN: 1471-2164

URL: http://www.biomedcentral.com/1471-

2164/3/27/abstract

DOI: 10.1186/1471-2164-3-27

PUB. COUNTRY:

United Kingdom

DOCUMENT TYPE:

Journal

LANGUAGE:

English

ENTRY DATE:

Entered STN: 20041108

Last Updated on STN: 20041108

AB Background: The objective of this research was to investigate the reproducibility of cross-species microarray hybridization. Comparisons between same- and cross-species hybridizations were also made. Nine hybridizations between a single pig skeletal muscle RNA sample and three human cDNA nylon microarrays were completed. Three replicate hybridizations of two different amounts of pig RNA, and of human skeletal muscle RNA were completed on three additional microarrays. Results: Reproducibility of microarray hybridizations of pig cDNA to human microarrays was high, as determined by Spearman and Pearson correlation coefficients and a Kappa statistic. Variability among replicate hybridizations was similar for human and pig data, indicating the reproducibility of results were not compromised in cross-species hybridized. The concordance between data generated from hybridizations using pig and human skeletal muscle RNA was high, further supporting the use of human microarrays for the analysis of gene expression in the pig. No systematic effect of stripping and reusing nylon microarrays was found, and variability across microarrays was minimal. Conclusion: The majority of genes generated highly reproducible data in cross-species microarray hybridizations, although approximately 6% were identified as highly variable. Experimental designs that include at least three replicate hybridizations for each experimental treatment will enable the variability of individual genes to be considered appropriately. The use of cross-species microarray analysis looks promising. However, additional validation is needed to determine the specificity of cross-species hybridizations, and the validity of results.

L6 ANSWER 1 OF 24 MEDLINE on STN ACCESSION NUMBER: 2003510296 MEDLINE PubMed ID: 12354330

DOCUMENT NUMBER: TITLE:

Cross-species hybridisation of pig RNA to human

nylon microarrays.

AUTHOR:

Moody D E; Zou Z; McIntyre L

CORPORATE SOURCE:

Department of Animal Science, 1151 Lilly Hall, Purdue

University, West Lafayette, IN 47907, USA...

moodyd@purdue.edu

SOURCE:

BMC genomics [electronic resource], (2002 Sep 27)

Vol. 3, No. 1, pp. 27. Electronic Publication: 2002-09-27. Journal code: 100965258. E-ISSN: 1471-2164.

PUB. COUNTRY:

England: United Kingdom

DOCUMENT TYPE:

Journal; Article; (JOURNAL ARTICLE)

LANGUAGE:

English

FILE SEGMENT:

NONMEDLINE; PUBMED-NOT-MEDLINE

ENTRY MONTH: 200310

ENTRY DATE:

Entered STN: 20031101

Last Updated on STN: 20031101

Entered Medline: 20031031

AB BACKGROUND: The objective of this research was to investigate the reproducibility of cross-species microarray hybridisation. Comparisons between same- and cross-species hybridisations were also made. Nine hybridisations between a single pig skeletal muscle RNA sample and three human cDNA nylon microarrays were completed. Three replicate hybridisations of two different amounts of pig RNA, and of human skeletal muscle RNA were completed on three additional microarrays. RESULTS: Reproducibility of microarray hybridisations of pig cDNA to human microarrays was high, as determined by Spearman and Pearson correlation coefficients and a Kappa statistic. Variability among replicate hybridisations was similar for human and pig data, indicating the reproducibility of results were not compromised in

cross-species hybridisations. The concordance between data generated from hybridisations using pig and human skeletal muscle RNA was high, further supporting the use of human microarrays for the analysis of gene expression in the pig. No systematic effect of stripping and re-using nylon microarrays was found, and variability across microarrays was minimal. CONCLUSION: The majority of genes generated highly reproducible data in cross-species microarray hybridisations, although approximately 6% were identified as highly variable. Experimental designs that include at least three replicate hybridisations for each experimental treatment will enable the variability of individual genes to be considered appropriately. The use of cross-species microarray analysis looks promising. However, additional validation is needed to determine the specificity of cross-species hybridisations, and the validity of results.

ANSWER 6 OF 24 MEDLINE on STN 2003010719 ACCESSION NUMBER: PubMed ID: 12517075 DOCUMENT NUMBER: TITLE: Generation of expressed sequence tags from a normalized porcine skeletal muscle cDNA library. AUTHOR: Yao Jianbo; Coussens Paul M; Saama Peter; Suchyta Steven; Ernst Catherine W CORPORATE SOURCE: Department of Animal Science and Center for Animal Functional Genomics, Michigan State University, East Lansing, MI 48824, USA.. yaoj@msu.edu SOURCE: Animal biotechnology, (2002 Nov) Vol. 13, No. 2, pp. 211-22. Journal code: 9011409. ISSN: 1049-5398. PUB. COUNTRY: United States Journal; Article; (JOURNAL ARTICLE) DOCUMENT TYPE: LANGUAGE: English FILE SEGMENT: Priority Journals OTHER SOURCE: GENBANK-BM189924; GENBANK-BM189925; GENBANK-BM189926; GENBANK-BM189927; GENBANK-BM189928; GENBANK-BM189929; GENBANK-BM189930; GENBANK-BM189931; GENBANK-BM189932; GENBANK-BM189933; GENBANK-BM189934; GENBANK-BM189935; GENBANK-BM189936; GENBANK-BM189937; GENBANK-BM189938; GENBANK-BM189939; GENBANK-BM189940; GENBANK-BM189941; GENBANK-BM189942; GENBANK-BM189943; GENBANK-BM189944; GENBANK-BM189945; GENBANK-BM189946; GENBANK-BM189947; GENBANK-BM189948; GENBANK-BM189949; GENBANK-BM189950; GENBANK-BM189951; GENBANK-BM189952; GENBANK-BM189953; GENBANK-BM189954; GENBANK-BM189955; GENBANK-BM189956; GENBANK-BM189957; GENBANK-BM189958; GENBANK-BM189959; GENBANK-BM189960; GENBANK-BM189961; GENBANK-BM189962; GENBANK-BM189963; GENBANK-BM189964; GENBANK-BM189965; GENBANK-BM189966; GENBANK-BM189967; GENBANK-BM189968; GENBANK-BM189969; GENBANK-BM189970; GENBANK-BM189971; GENBANK-BM189972; GENBANK-BM189973; GENBANK-BM189974; GENBANK-BM189975; GENBANK-BM189976; GENBANK-BM189977; GENBANK-BM189978; GENBANK-BM189979; GENBANK-BM189980; GENBANK-BM189981; GENBANK-BM189982; GENBANK-BM189983; GENBANK-BM189984; GENBANK-BM189985; GENBANK-BM189986; GENBANK-BM189987; GENBANK-BM189988; GENBANK-BM189989; GENBANK-BM189990; GENBANK-BM189991; GENBANK-BM189992; GENBANK-BM189993; GENBANK-BM189994; GENBANK-BM189995; GENBANK-BM189996; GENBANK-BM189997; GENBANK-BM189998; GENBANK-BM189999; GENBANK-BM190000; GENBANK-BM190001; GENBANK-BM190002; GENBANK-BM190003; GENBANK-BM190004; GENBANK-BM190005; GENBANK-BM190006; GENBANK-BM190007; GENBANK-BM190008; GENBANK-BM190009; GENBANK-BM190010; GENBANK-BM190011; GENBANK-BM190012; GENBANK-BM190013;

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AΒ Recent developments in microarray technologies permit scientists to analyze expression of thousands of genes simultaneously in diverse biological systems. In an effort to provide integrated resources for application of microarray technologies to studies of skeletal muscle growth and development in swine, we have constructed a normalized cDNA library from porcine skeletal muscle. The effectiveness of normalization was evaluated by DNA sequencing of clones randomly picked from the library before and after normalization, and also by Southern blot hybridization using probes representing abundant transcripts. Our data suggests that the normalization procedure successfully reduced the highly abundant cDNA species in the normalized library. To date, a total of 782 EST (expressed sequence tag) sequences have been generated from this normalized library (687 ESTs) and the original library (95 ESTs). The sequence information of these ESTs plus their BLAST results has been made available through a web accessible database (http://nbfgc.msu.edu). Cluster analysis of the data indicates that a total of 742 unique sequences are present in this collection. BLASTN search of the 742 EST sequences against the public database (dbEST) revealed that 139 had no significant matches (E-value > 10(-15)) to porcine ESTs already entered in the database, suggesting the possibility of their specific expression in porcine skeletal muscle. Generation of

non-redundant ESTs from this library will allow us to construct cDNA microarrays for identification of gene expression changes that regulate muscle growth and affect meat quality in swine.

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ACCESSION NUMBER: 2003:154606 BIOSIS DOCUMENT NUMBER: PREV200300154606

TITLE: A Comparison of **Porcine** Ocular Tissue Gene

Expression by Microarray Analysis.

AUTHOR(S): La Morticella, D. M. [Reprint Author]; Samples, J. R.

[Reprint Author]; Rust, K. C. [Reprint Author]; Acott, T.

S. [Reprint Author]; Wirtz, M. K. [Reprint Author]

CORPORATE SOURCE: Ophthalmology, Casey Eye Institute, Portland, OR, USA

SOURCE: ARVO Annual Meeting Abstract Search and Program Planner, (

2002) Vol. 2002, pp. Abstract No. 2436. cd-rom. Meeting Info.: Annual Meeting of the Association For Research in Vision and Ophthalmology. Fort Lauderdale,

Florida, USA. May 05-10, 2002.

DOCUMENT TYPE: Conference; (Meeting)

Conference; Abstract; (Meeting Abstract)

LANGUAGE: English

ENTRY DATE: Entered STN: 26 Mar 2003

Last Updated on STN: 26 Mar 2003

AB Purpose: Microarray analysis was used to determine if porcine cDNA would hybridize cleanly to human

cDNA arrays. Gene expression from ocular tissues was

measured and compared to help elucidate their functions. It was sought to determine if unique gene upregulation in different ocular tissues occurs, and if so what genes are involved. Methods: Total RNA was extracted from porcine iris, cilliary body, retina, and optic nerve tissues.

Labeled cDNA was generated using the Perkin Elmer TSA kit.

Samples were hybridized to human cDNA microarrays

containing 5700 PCR products spotted in duplicate. Amplicons making up the arrays are genes or ESTs, and are amplified from ResGen

human library clones. Labeled cilliary body, optic nerve, and retina cDNA were each hybridized separately with labeled iris

cDNA on two double spotted arrays. Results: It was

found that there are genes which are upregulated uniquely in each of the ocular tissues studied. Cilliary body uniquely upregulated genes included lysyl oxidase - likel (LOXL1), ATP1 B3 ATPase, Na+/K+ transporting, beta 3 polypeptide, FMOD Fibromodulin, GPNMB Glycoprotein (transmembrane) nmb, and OAT Ornithine aminotrasferase (gyrate atrophy). In Iris Beta Al Crystallin (CRYBA1), and Actin gamma 2 smooth muscle enteric (ACTG2) were uniquely upregulated. Myelin Basic Protein (MBP), Proteolipid protein 1 (PLP1) Myelin - associated oligodendrocyte basic

Proteolipid protein 1 (PLP1), Myelin - associated oligodendrocyte basic protein (MOBP), and S100 calcium - binding protein beta (SB100) were unique to optic nerve. In Retinal tissue CKMT2 creatine kinase mitochondrial 2 (sarcomeric), UNC119 (c. elegans) homolog, and ATPB2 ATPase Na+/K+ transporting beta 2 polypeptide were found to be uniquely

upregulated. Conclusion: Upregulated genes in **porcine** ocular tissues could be determined by **microarray** analysis with

SMChum5700 human cDNA arrays from the Spotted

Microarray Core at Oregon Health and Science University. Genes that are upregulated specific to tissue type are able to be determined using these arrays.

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#84	Search Identification of differential expression ESTs in pig muscle Limits: Publication Date from 1980 to 2003	15:25:25	1
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